

REMARKS

Applicant hereby submits a sequence listing containing the nucleic acid and amino acid sequences as filed in the figures of the present continuing application. Applicant notes that the present application claims priority from patent application Serial No. 09/259,214 ('214), filed March 1, 1999, which is a Divisional of patent application Serial No. 08/910,798 ('798), filed August 13, 1997, now U.S. Patent No. 5,876,997 ('997), issued March 2, 1999. Applicant further notes that the sequence listing filed in the '798 application, and issued in the '997 patent, inadvertently omitted a portion of the nucleic acid sequence for SEQ ID NO:1 and the corresponding amino acid sequence for SEQ ID NO:2. The full and correct sequence is contained in Figure 1 of the '798 application as filed and in Figure 1A and 1B of the '997 patent issued therefrom. The present continuation application is intended to claim the invention as originally disclosed in Figure 1 of the priority application.

Below, Applicant has provided the corrected SEQ ID NO:1 and 2 and has boldfaced the nucleic acid sequence and amino acid sequence inadvertently omitted from each. Applicant notes that nucleotides 357-408 have been added to SEQ ID NO:1 to correspond to originally filed Figure 1. Applicant further notes that amino acids 120-135 have been added to SEQ ID NO:2 to correspond to originally filed Figure 1.

<210> 1
<211> 1323
<212> DNA
<213> Escherichia coli
<220>
<221> CDS
<222> (1) .. (1323)
<400> 1

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Met	Lys	Ala	Ile	Leu	Ile	Pro	Phe	Leu	Ser	Leu	Leu	Ile	Pro	Leu	Thr	
1				5					10					15		
ccg	caa	tct	gca	ttc	gct	cag	agt	gag	ccg	gag	ctg	aag	ctg	gaa	agt	96
Pro	Gln	Ser	Ala	Phe	Ala	Gln	Ser	Glu	Pro	Glu	Leu	Lys	Leu	Glu	Ser	
			20					25					30			
gtg	gtg	att	gtc	agt	cgt	cat	ggt	gtg	cgt	gct	cca	acc	aag	gcc	acg	144
Val	Val	Ile	Val	Ser	Arg	His	Gly	Val	Arg	Ala	Pro	Thr	Lys	Ala	Thr	
			35				40					45				
caa	ctg	atg	cag	gat	gtc	acc	cca	gac	gca	tgg	cca	acc	tgg	ccg	gta	192
Gln	Leu	Met	Gln	Asp	Val	Thr	Pro	Asp	Ala	Tyr	Pro	Thr	Trp	Pro	Val	
	50					55				60						
aaa	ctg	ggt	tgg	ctg	aca	ccg	cgn	ggt	ggt	gag	cta	atc	gcc	tat	ctc	240
Lys	Leu	Gly	Trp	Leu	Thr	Pro	Xaa	Gly	Gly	Glu	Leu	Ile	Ala	Tyr	Leu	

65	70	75	80	
gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg gcg aaa	288			
Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys				
85 90 95				
aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat gtc gac	336			
Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp				
100 105 110				
gag cgt acc cgt aaa aca ggc gaa gcc ttc gcc gcc ggg ctg gca cct	384			
Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro				
115 120 125				
gac tgt gca ata acc gta cat acc cag gca gat acg tcc agt ccc gat	432			
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp				
130 135 140				
ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat aac gcg	480			
Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala				
145 150 155 160				
aac gtg act gac gcg atc ctc agc agg gca gga ggg tca att gct gac	528			
Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp				
165 170 175				
ttt acc ggg cat cgg caa acg gcg ttt cgc gaa ctg gaa cgg gtg ctt	576			
Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu				
180 185 190				
aat ttt ccg caa tca aac ttg tgc ctt aaa cgt gag aaa cag gac gaa	624			
Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu				
195 200 205				
agc tgt tca tta acg cag gca tta cca tcg gaa ctc aag gtg agc gcc	672			
Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala				
210 215 220				
gac aat gtc tca tta acc ggt gcg gta agc ctc gca tca atg ctg acg	720			
Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr				
225 230 235 240				
gag ata ttt ctc ctg caa caa gca cag gga atg ccg gag ccg ggg tgg	768			
Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp				
245 250 255				
gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt ttg cat	816			
Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His				
260 265 270				
aac gcg caa ttt tat ttg cta caa cgc acg cca gag gtt gcc cgc agc	864			
Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser				
275 280 285				
cgc gcc acc ccg tta ttg gat ttg atc atg gca gcg ttg acg ccc cat	912			
Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His				
290 295 300				
cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca gta ctg	960			
Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu				
305 310 315 320				

ttt att gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg	1008
Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu	
325 330 335	

gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt	1056
Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly	
340 345 350	

ggt gaa ctg gtg ttt gaa cgc tgg cgt ccg cta agc gat aac agc cag	1104
Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln	
355 360 365	

tgg att cag gtt tct ctg gtc ttc cag act tta cag cag atg cgt gat	1152
Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp	
370 375 380	

aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc	1200
Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr	
385 390 395 400	

ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tct ttg gca	1248
Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala	
405 410 415	

ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg	1296
Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu	
420 425 430	

aga tct cat cac cat cac cat cac taa	1323
Arg Ser His His His His His His	
435 440	

<210> 2
 <211> 440
 <212> PRT
 <213> Escherichia coli
 <400> 2

Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr
1 5 10 15

Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
20 25 30

Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
35 40 45

Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
50 55 60

Lys Leu Gly Trp Leu Thr Pro Xaa Gly Gly Glu Leu Ile Ala Tyr Leu
65 70 75 80

Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
85 90 95

Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
100 105 110

A

Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
 115 120 125
 Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
 130 135 140
 Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
 145 150 155 160
 Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp
 165 170 175
 Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu
 180 185 190
 Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu
 195 200 205
 Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
 210 215 220
 Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
 225 230 235 240
 Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
 245 250 255
 Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
 260 265 270
 Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
 275 280 285
 Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His
 290 295 300
 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
 305 310 315 320
 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
 325 330 335
 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
 340 345 350
 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
 355 360 365
 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
 370 375 380
 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
 385 390 395 400
 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
 405 410 415
 Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
 420 425 430
 Arg Ser His His His His His His
 435 440

Below, Applicant has provided the SEQ ID NO:1 and 2 from the sequence listing filed in the '798 application, and issued in the '997 patent. Applicant notes that nucleotides 357-408 were inadvertently omitted from SEQ ID NO:1 as indicated by the underlined sequence. Applicant further notes that amino acids 120-135 were inadvertently omitted from SEQ ID NO:2 as indicated by the underlined sequence.

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: PHYTASE
- (ix) FEATURE:
 - (A) NAME/KEY:
 - (B) LOCATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG AAA GCG ATC TTA ATC CCA TTT TTA TCT CTT CTG ATT CCG TTA ACC	48
Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr	
1 5 10 15	
CCG CAA TCT GCA TTC GCT CAG AGT GAG CCG GAG CTG AAG CTG GAA AGT	96
Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser	
20 25 30	
GTG GTG ATT GTC AGT CGT CAT GGT GTG CGT GCT CCA ACC AAG GCC ACG	144
Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr	
35 40 45	
CAA CTG ATG CAG GAT GTC ACC CCA GAC GCA TCG CCA ACC TGG CCG GTA	192
Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val	
50 55 60	
AAA CTG GGT TGG CTG ACA CCG CGN GGT GGT GAG CTA ATC GCC TAT CTC	240
Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu	
65 70 75 80	
GGA CAT TAC CAA CGC CAG CGT CTG GTA GCC GAC GGA TTG CTG GCG AAA	288
Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys	
85 90 95	
AAG GGC TGC CCG CAG TCT GGT CAG GTC GCG ATT ATT GCT GAT GTC GAC	336
Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp	
100 105 110	
GAG CGT ACC CGT AAA ACA <u>GGC CAG</u> GCA GAT ACG TCC AGT CCC GAT CCG	384
Glu Arg Thr Arg Lys Thr <u>Gly Gln</u> Ala Asp Thr Ser Ser Pro Asp Pro	
115 120 125	
TTA TTT AAT CCT CTA AAA ACT GGC GTT TGC CAA CTG GAT AAC GCG AAC	432
Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn	
130 135 140	

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GTG	ACT	GAC	GCG	ATC	CTC	AGC	AGG	GCA	GGA	GCG	TCA	ATT	GCT	GAC	TTT	480
Val	Thr	Asp	Ala	Ile	Leu	Ser	Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp	Phe	
145					150					155					160	
ACC	GGG	CAT	CGG	CAA	ACG	GCG	TTT	CGC	GAA	CTG	GAA	CGG	GTG	CTT	AAT	528
Thr	Gly	His	Arg	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu	Asn	
				165					170					175		
TTT	CCG	CAA	TCA	AAC	TTG	TGC	CTT	AAA	CGT	GAG	AAA	CAG	GAC	GAA	AGC	576
Phe	Pro	Gln	Ser	Asn	Leu	Cys	Leu	Lys	Arg	Glu	Lys	Gln	Asp	Glu	Ser	
			180					185					190			
TGT	TCA	TTA	ACG	CAG	GCA	TTA	CCA	TCG	GAA	CTC	AAG	GTG	AGC	GCC	GAC	624
Cys	Ser	Leu	Thr	Gln	Ala	Leu	Pro	Ser	Glu	Leu	Lys	Val	Ser	Ala	Asp	
		195					200					205				
AAT	GTC	TCA	TTA	ACC	GGT	GCG	GTA	AGC	CTC	GCA	TCA	ATG	CTG	ACG	GAG	672
Asn	Val	Ser	Leu	Thr	Gly	Ala	Val	Ser	Leu	Ala	Ser	Met	Leu	Thr	Glu	
	210					215					220					
ATA	TTT	CTC	CTG	CAA	CAA	GCA	CAG	GGA	ATG	CCG	GAG	CCG	GGG	TGG	GGA	720
Ile	Phe	Leu	Leu	Gln	Gln	Ala	Gln	Gly	Met	Pro	Glu	Pro	Gly	Trp	Gly	
225					230					235				240		
AGG	ATC	ACC	GAT	TCA	CAC	CAG	TGG	AAC	ACC	TTG	CTA	AGT	TTG	CAT	AAC	768
Arg	Ile	Thr	Asp	Ser	His	Gln	Trp	Asn	Thr	Leu	Leu	Ser	Leu	His	Asn	
				245				250						255		
GCG	CAA	TTT	TAT	TTG	CTA	CAA	CGC	ACG	CCA	GAG	GTT	GCC	CGC	AGC	CGC	816
Ala	Gln	Phe	Tyr	Leu	Leu	Gln	Arg	Thr	Pro	Glu	Val	Ala	Arg	Ser	Arg	
			260				265						270			
GCC	ACC	CCG	TTA	TTG	GAT	TTG	ATC	ATG	GCA	GCG	TTG	ACG	CCC	CAT	CCA	864
Ala	Thr	Pro	Leu	Leu	Asp	Leu	Ile	Met	Ala	Ala	Leu	Thr	Pro	His	Pro	
		275					280					285				
CCG	CAA	AAA	CAG	GCG	TAT	GGT	GTG	ACA	TTA	CCC	ACT	TCA	GTA	CTG	TTT	912
Pro	Gln	Lys	Gln	Ala	Tyr	Gly	Val	Thr	Leu	Pro	Thr	Ser	Val	Leu	Phe	
	290					295					300					
ATT	GCC	GGA	CAC	GAT	ACT	AAT	CTG	GCA	AAT	CTC	GGC	GGC	GCA	CTG	GAG	960
Ile	Ala	Gly	His	Asp	Thr	Asn	Leu	Ala	Asn	Leu	Gly	Gly	Ala	Leu	Glu	
305					310					315				320		
CTC	AAC	TGG	ACG	CTT	CCC	GGT	CAG	CCG	GAT	AAC	ACG	CCG	CCA	GGT	GGT	1008
Leu	Asn	Trp	Thr	Leu	Pro	Gly	Gln	Pro	Asp	Asn	Thr	Pro	Pro	Gly	Gly	
				325				330						335		
GAA	CTG	GTG	TTT	GAA	CGC	TGG	CGT	CGG	CTA	AGC	GAT	AAC	AGC	CAG	TGG	1056
Glu	Leu	Val	Phe	Glu	Arg	Trp	Arg	Arg	Leu	Ser	Asp	Asn	Ser	Gln	Trp	
			340					345					350			
ATT	CAG	GTT	TCG	CTG	GTC	TTC	CAG	ACT	TTA	CAG	CAG	ATG	CGT	GAT	AAA	1104
Ile	Gln	Val	Ser	Leu	Val	Phe	Gln	Thr	Leu	Gln	Gln	Met	Arg	Asp	Lys	
		355					360					365				
ACG	CCG	CTG	TCA	TTA	AAT	ACG	CCG	CCC	GGA	GAG	GTG	AAA	CTG	ACC	CTG	1152
Thr	Pro	Leu	Ser	Leu	Asn	Thr	Pro	Pro	Gly	Glu	Val	Lys	Leu	Thr	Leu	
		370				375					380					

GCA GGA TGT GAA GAG CGA AAT GCG CAG GGC ATG TGT TCG TTG GCA GGT 1200
 Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly
 385 390 395 400

TTT ACG CAA ATC GTG AAT GAA GCA CGC ATA CCG GCG TGC AGT TTG AGA 1248
 Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu Arg
 405 410 415

TCT CAT CAC CAT CAC CAT CAC TAA 1272
 Ser His His His His His His
 420

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr
 1 5 10 15
 Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
 20 25 30
 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
 35 40 45
 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
 50 55 60
 Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
 65 70 75 80
 Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
 85 90 95
 Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
 100 105 110
 Glu Arg Thr Arg Lys Thr Gly Gln Ala Asp Thr Ser Ser Pro Asp Pro
 115 120 125
 Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn
 130 135 140
 Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp Phe
 145 150 155 160
 Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn
 165 170 175
 Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser
 180 185 190
 Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp
 195 200 205
 Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu
 210 215 220
 Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp Gly
 225 230 235 240
 Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His Asn
 245 250 255
 Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
 260 265 270
 Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His Pro
 275 280 285
 Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe
 290 295 300

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Ile	Ala	Gly	His	Asp	Thr	Asn	Leu	Ala	Asn	Leu	Gly	Gly	Ala	Leu	Glu
305					310					315					320
Leu	Asn	Trp	Thr	Leu	Pro	Gly	Gln	Pro	Asp	Asn	Thr	Pro	Pro	Gly	Gly
				325					330					335	
Glu	Leu	Val	Phe	Glu	Arg	Trp	Arg	Arg	Leu	Ser	Asp	Asn	Ser	Gln	Trp
			340					345					350		
Ile	Gln	Val	Ser	Leu	Val	Phe	Gln	Thr	Leu	Gln	Gln	Met	Arg	Asp	Lys
		355					360					365			
Thr	Pro	Leu	Ser	Leu	Asn	Thr	Pro	Pro	Gly	Glu	Val	Lys	Leu	Thr	Leu
	370					375					380				
Ala	Gly	Cys	Glu	Glu	Arg	Asn	Ala	Gln	Gly	Met	Cys	Ser	Leu	Ala	Gly
385					390					395					400
Phe	Thr	Gln	Ile	Val	Asn	Glu	Ala	Arg	Ile	Pro	Ala	Cys	Ser	Leu	Arg
				405			410						415		
Ser	His	His	His	His	His	His									
			420												

Applicant respectfully requests entry of this preliminary amendment. Applicant further requests entry of the sequence listing which accompanies the present amendment beginning on page 33 of the specification and numbering consecutively thereafter. The new sequence listing has been revised, as compared to the issued '997 patent, to reflect the nucleic acid and amino acid sequences disclosed in the specification and figures of the present application. No new matter has been added. Claims 1-9 are pending and at issue. Applicant respectfully requests reconsideration of the present application.

If the Examiner would like to discuss any of the issues raised in this preliminary amendment, Applicant's representative can be reached at (619) 678-5070. Please charge any additional fees, or make any credits, to Deposit Account No. 06-1050.

Respectfully submitted,

Date: 4/13/99


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